

Shak

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/519,559

Source: Pur/10

Date Processed by STIC: 11/16/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 11/16/2005

PATENT APPLICATION: US/10/519,559

TIME: 08:17:06

Input Set : N:\Rasheed\PTO.SR.txt

Output Set: N:\CRF4\11162005\J519559.raw

4 <110> APPLICANT: Japan Science and Technology Corporation
 6 <120> TITLE OF INVENTION: Hollow nano-particles composed of cysteine-modified proteins, and their
 7 use as a therapeutic drug
 9 <130> FILE REFERENCE: P023P05US(PCT)
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/519,559
 C--> 11 <141> CURRENT FILING DATE: 2004-12-28
 11 <150> PRIOR APPLICATION NUMBER: JP2002-191386
 W--> 12 <151> PRIOR FILING DATE: 2002-6-28
 W--> 14 <150> PRIOR APPLICATION NUMBER:
 W--> 15 <151> PRIOR FILING DATE: 2003-6-27
 17 <160> NUMBER OF SEQ ID NOS: 36
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1218
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Hepatitis B virus
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)..(1218)
 30 <400> SEQUENCE: 1
 31 atg aga tct ttg ttg atc ttg gtt ttg tgt ttc ttg cca ttg gct gct 48
 32 Met Arg Ser Leu Leu Ile Leu Val Leu Cys Phe Leu Pro Leu Ala Ala
 33 1 5 10 15
 35 ttg ggt aag gtt cga caa ggc atg ggg acg aat ctt tct gtt ccc aat 96
 36 Leu Gly Lys Val Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro Asn
 37 20 25 30
 39 cct ctg gga ttc ttt ccc gat cac cag ttg gac cct gcg ttc gga gcc 144
 40 Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala
 41 35 40 45
 43 aac tca aac aat cca gat tgg gac ttc aac ccc aac aag gat caa tgg 192
 44 Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp Gln Trp
 45 50 55 60
 47 cca gag gca aat cag gta gga gcg gga gca ttc ggg cca ggg ttc acc 240
 48 Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly Pro Gly Phe Thr
 49 65 70 75 80
 51 cca cca cac ggc ggt ctt ttg ggg tgg agc cct cag gct cag ggc ata 288
 52 Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile
 53 85 90 95
 55 ttg aca aca gtg cca gca gca cct cct cct gcc tcc acc aat cgg cag 336
 56 Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser Thr Asn Arg Gln
 57 100 105 110
 59 tca gga aga cag cct act ccc atc tct cca cct cta aga gac agt cat 384
 60 Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg Asp Ser His

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61	115	120	125	
63	cct cag gcc atg cag tgg aat tcc aca aca ttc cac caa gct ctg cta	432		
64	Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu			
65	130	135	140	
67	gat ccc aga gtg agg ggc cta tat ttt cct gct ggt ggc tcc agt tcc	480		
68	Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser			
69	145	150	155	160
71	gga aca gta aac cct gtt ccg act act gcc tca ccc ata tct ggg gac	528		
72	Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Gly Asp			
73	165	170	175	
75	cct gca ccg aac atg gag aac aca aca tca gga ttc cta gga ccc ctg	576		
76	Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu			
77	180	185	190	
79	ctc gtg tta cag gcg ggg ttt ttc ttg ttg aca aga atc ctc aca ata	624		
80	Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile			
81	195	200	205	
83	cca cag agt cta gac tcg tgg tgg act tct ctc aat ttt cta ggg gga	672		
84	Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly			
85	210	215	220	
87	gca ccc acg tgt cct ggc caa aat tcg cag tcc cca acc tcc aat cac	720		
88	Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His			
89	225	230	235	240
91	tca cca acc tct tgt cct cca att tgt cct ggc tat cgc tgg atg tgt	768		
92	Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys			
93	245	250	255	
95	ctg cgg cgt ttt atc ata ttc ctc ttc atc ctg ctg cta tgc ctc atc	816		
96	Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile			
97	260	265	270	
99	ttc ttg ttg gtt ctt ctg gac tac caa ggt atg ttg ccc gtt tgt cct	864		
100	Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro			
101	275	280	285	
103	cta ctt cca gga aca tca acc acc agc acg ggg cca tgc aag acc tgc	912		
104	Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys			
105	290	295	300	
107	acg att cct gct caa gga acc tct atg ttt ccc tct tgt tgc tgt aca	960		
108	Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr			
109	305	310	315	320
111	aaa cct tcg gac gga aac tgc act tgt att ccc atc cca tca tcc tgg	1008		
112	Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp			
113	325	330	335	
115	gct ttc gca aga ttc cta tgg gag tgg gcc tca gtc cgt ttc tcc tgg	1056		
116	Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp			
117	340	345	350	
119	ctc agt tta cta gtg cca ttt gtt cag tgg ttc gta ggg ctt tcc ccc	1104		
120	Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro			
121	355	360	365	
123	act gtt tgg ctt tca gtt ata tgg atg atg tgg tat tgg ggg cca agt	1152		
124	Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser			
125	370	375	380	

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127 ctg tac aac atc ttg agt ccc ttt tta cct cta tta cca att ttc ttt      1200
128 Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
129 385                               390                               395          400
131 tgt ctt tgg gta tat att                                          1218
132 Cys Leu Trp Val Tyr Ile
133                               405
136 <210> SEQ ID NO: 2
137 <211> LENGTH: 406
138 <212> TYPE: PRT
139 <213> ORGANISM: Hepatitis B virus
141 <400> SEQUENCE: 2
142 Met Arg Ser Leu Leu Ile Leu Val Leu Cys Phe Leu Pro Leu Ala Ala
143   1                               5                               10              15
145 Leu Gly Lys Val Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro Asn
146                               20                               25              30
148 Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala
149                               35                               40              45
151 Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp Gln Trp
152   50                               55                               60
154 Pro Glu Ala Asn Gln Val Gly Ala Gly Ala Phe Gly Pro Gly Phe Thr
155   65                               70                               75              80
157 Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile
158                               85                               90              95
160 Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser Thr Asn Arg Gln
161                               100                              105              110
163 Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg Asp Ser His
164                               115                              120              125
166 Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
167   130                              135                              140
169 Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser
170 145                              150                              155              160
172 Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro Ile Ser Gly Asp
173                               165                              170              175
175 Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu
176                               180                              185              190
178 Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile
179                               195                              200              205
181 Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly
182   210                              215                              220
184 Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His
185 225                              230                              235              240
187 Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys
188                               245                              250              255
190 Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile
191                               260                              265              270
193 Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro
194   275                              280                              285
196 Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys
197   290                              295                              300

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199 Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr
200 305                      310                      315                      320
202 Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp
203                      325                      330                      335
205 Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp
206                      340                      345                      350
208 Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro
209                      355                      360                      365
211 Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser
212                      370                      375                      380
214 Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe
215 385                      390                      395                      400
217 Cys Leu Trp Val Tyr Ile
218                      405
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 26
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
229     Synthesized Primer Sequence
231 <400> SEQUENCE: 3
232 gcacccacgt ctctggcca aaattc                      26
235 <210> SEQ ID NO: 4
236 <211> LENGTH: 26
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
242     Synthesized Primer Sequence
244 <400> SEQUENCE: 4
245 gaattttggc caggagacgt ggggtgc                      26
248 <210> SEQ ID NO: 5
249 <211> LENGTH: 26
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
255     Synthesized Primer Sequence
257 <400> SEQUENCE: 5
258 tcaccaacct ctagtcctcc aatttg                      26
261 <210> SEQ ID NO: 6
262 <211> LENGTH: 26
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
268     Synthesized Primer Sequence
270 <400> SEQUENCE: 6

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RAW SEQUENCE LISTING

DATE: 11/16/2005

PATENT APPLICATION: US/10/519,559

TIME: 08:17:06

Input Set : N:\Rasheed\PTO.SR.txt

Output Set: N:\CRF4\11162005\J519559.raw

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271 caaattggag gactagaggt tggatga                26
274 <210> SEQ ID NO: 7
275 <211> LENGTH: 28
276 <212> TYPE: DNA
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
281     Synthesized Primer Sequence
283 <400> SEQUENCE: 7
284 cttgtcctcc aataagtcct ggctatcg                28
287 <210> SEQ ID NO: 8
288 <211> LENGTH: 28
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
294     Synthesized Primer Sequence
296 <400> SEQUENCE: 8
297 cgatagccag gacttattgg aggacaag                28
300 <210> SEQ ID NO: 9
301 <211> LENGTH: 30
302 <212> TYPE: DNA
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
307     Synthesized Primer Sequence
309 <400> SEQUENCE: 9
310 tategctgga tggcgctgcg gcgttttata                30
313 <210> SEQ ID NO: 10
314 <211> LENGTH: 30
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial Sequence
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
320     Synthesized Primer Sequence
322 <400> SEQUENCE: 10
323 aaaacgccgc agcgccatcc agcgatagcc                30
326 <210> SEQ ID NO: 11
327 <211> LENGTH: 28
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of Artificial Sequence:Artificially
333     Synthesized Primer Sequence
335 <400> SEQUENCE: 11
336 catcctgctg ctaccctca tcttcttg                28
339 <210> SEQ ID NO: 12
340 <211> LENGTH: 28
341 <212> TYPE: DNA

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/519,559

DATE: 11/16/2005

TIME: 08:17:07

Input Set : N:\Rasheed\PTO.SR.txt

Output Set: N:\CRF4\11162005\J519559.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:14 M:256 W: Invalid Numeric Header Field, <150> PRIOR APPLICATION NUMBER:
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD